

SEQUENCE LISTING

<110> KANNO , SOHEI  
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NAKAMATSU, TSUYOSHI  
KIMURA, EIICHIRO

<120> ABC TRANSPORTER AND GENE CODING FOR THE SAME

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<140> US09/868338

<141> 2001-06-18

<150> JP 10/360621

<151> 1998-12-18

<150> PCT/JP 99/07079

<151> 1998-12-18

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<170> PatentIn version 3.1

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Met	Leu	Ala	Thr	Arg	Leu	Ile	Thr	Leu	Phe	Phe	Phe	Leu	Gly	Ile	Ile	
1				5				10					15			

gga	tcg	cta	acc	ggt	aac	ctc	agt	gaa	cta	cgt	gca	caa	act	act	ttt	96
Gly	Ser	Leu	Thr	Gly	Asn	Leu	Ser	Glu	Leu	Arg	Ala	Gln	Thr	Thr	Phe	
			20					25					30			

agt	aca	tta	tgg	gat	acc	cat	aaa	gaa	acc	tat	aga	gtc	tcc	ata	gct	144
Ser	Thr	Leu	Trp	Asp	Thr	His	Lys	Glu	Thr	Tyr	Arg	Val	Ser	Ile	Ala	
		35				40					45					

tcc	gca	gca	gga	caa	gac	ttc	tac	ggg	ctt	gct	gag	act	cta	cgc	act	192
Ser	Ala	Ala	Gly	Gln	Asp	Phe	Tyr	Gly	Leu	Ala	Glu	Thr	Leu	Arg	Thr	
	50					55					60					

atg	gat	agg	cat	ggg	gaa	att	att	ttg	gca	gat	cgt	caa	tgg	tta	aca	240
Met	Asp	Arg	His	Gly	Glu	Ile	Ile	Leu	Ala	Asp	Arg	Gln	Trp	Leu	Thr	
65					70				75					80		

gct	ccc	ctt	gat	atc	ggt	gca	cca	gtc	gta	tta	tca	aac	aca	act	ttt	288
Ala	Pro	Leu	Asp	Ile	Gly	Ala	Pro	Val	Val	Leu	Ser	Asn	Thr	Thr	Phe	
				85				90						95		

gcc	gtt	gat	gaa	gga	cta	ctt	gcg	cca	aaa	gat	cta	ccg	caa	agt	gac	336
Ala	Val	Asp	Glu	Gly	Leu	Leu	Ala	Pro	Lys	Asp	Leu	Pro	Gln	Ser	Asp	
			100					105					110			

gag atc aca ata ttg cat cct cag ttt ctg gat tcg gcc aaa gag cca	384
Glu Ile Thr Ile Leu His Pro Gln Phe Leu Asp Ser Ala Lys Glu Pro	
115 120 125	
gaa tta ctt ggt ttg ctg gag ttc gaa gca tcc aac tca caa gtg cca	432
Glu Leu Leu Gly Leu Leu Glu Phe Glu Ala Ser Asn Ser Gln Val Pro	
130 135 140	
atg cca aag atc caa agc att cca tat gat agc gaa gac tca acc aac	480
Met Pro Lys Ile Gln Ser Ile Pro Tyr Asp Ser Glu Asp Ser Thr Asn	
145 150 155 160	
ccc atg tct gaa gtt ttt acc tac aac att aac ctg gat agt gca gta	528
Pro Met Ser Glu Val Phe Thr Tyr Asn Ile Asn Leu Asp Ser Ala Val	
165 170 175	
aga aac cca atc gta gtt atc ctt ccc gca ggc tta gag ctt tta agt	576
Arg Asn Pro Ile Val Val Ile Leu Pro Ala Gly Leu Glu Leu Leu Ser	
180 185 190	
gat caa aat ttg tcg gct cga ctc aca cag aat agt ctg ctg ata aaa	624
Asp Gln Asn Leu Ser Ala Arg Leu Thr Gln Asn Ser Leu Leu Ile Lys	
195 200 205	
gac cag act ggt gtg aac gct ctt cta tcc tca gag gat tca cgc aat	672
Asp Gln Thr Gly Val Asn Ala Leu Leu Ser Ser Glu Asp Ser Arg Asn	
210 215 220	
tat gtg gga gct gca tcc ccg atg att gac acg tgg gaa gaa agc gtt	720
Tyr Val Gly Ala Ala Ser Pro Met Ile Asp Thr Trp Glu Glu Ser Val	
225 230 235 240	
gtt cgg ttg aag gaa gcg aac caa ata atc gcc ttc aac gct ttc att	768
Val Arg Leu Lys Glu Ala Asn Gln Ile Ile Ala Phe Asn Ala Phe Ile	
245 250 255	
gca ttg ttc ctc acg acg act ctt gtt cta gca tac tgc act ggt att	816
Ala Leu Phe Leu Thr Thr Thr Leu Val Leu Ala Tyr Cys Thr Gly Ile	
260 265 270	
tca ttt aag aaa tca aag aag act atg ggt agc gca tct act agg aaa	864
Ser Phe Lys Lys Ser Lys Lys Thr Met Gly Ser Ala Ser Thr Arg Lys	
275 280 285	
tca tcc att aag agc tcg att aca gct gct aat tgt aga agt aat ttt	912
Ser Ser Ile Lys Ser Ser Ile Thr Ala Ala Asn Cys Arg Ser Asn Phe	
290 295 300	
cgc ttc aat tcc gtg cgt ctg gct cgc gaa ccg cta ttt cga gcg atc	960
Arg Phe Asn Ser Val Arg Leu Ala Arg Glu Pro Leu Phe Arg Ala Ile	
305 310 315 320	
tgc agc aat agc ttc aga tgc tcc ctc agc cag ata ctt aga aca tct	1008
Cys Ser Asn Ser Phe Arg Cys Ser Leu Ser Gln Ile Leu Arg Thr Ser	
325 330 335	

05060338 061301

caa ttc tat acc tcc atc act gcc gtt ggt ttt agg aat ctt aat aat	1056
Gln Phe Tyr Thr Ser Ile Thr Ala Val Gly Phe Arg Asn Leu Asn Asn	
340 345 350	
cggttg gac ttc act ttc att ttt cag ttc gat gaa gct tcc ttt	1101
Arg Leu Asp Phe Thr Phe Ile Phe Gln Phe Asp Glu Ala Ser Phe	
355 360 365	
tgaaaagagc acaca atg ata gaa atc aat gac ctc aag aaa tct ttt ggc	1152
Met Ile Glu Ile Asn Asp Leu Lys Lys Ser Phe Gly	
370 375	
gtt cgg atc tta tgg caa ggt ctc agt cat aag ttt tta cca gga aca	1200
Val Arg Ile Leu Trp Gln Gly Leu Ser His Lys Phe Leu Pro Gly Thr	
380 385 390 395	
atg aca gca ctg act gga gcg tcc ggt tca gga aaa tcg act ttg ctc	1248
Met Thr Ala Leu Thr Gly Ala Ser Gly Ser Gly Lys Ser Thr Leu Leu	
400 405 410	
aac tgt ctt ggc aca ctt gac aaa cca agt tcc gga cag atc ctt gtc	1296
Asn Cys Leu Gly Thr Leu Asp Lys Pro Ser Ser Gly Gln Ile Leu Val	
415 420 425	
gag gat gta gac ctt ctg aaa ctc tct acg cgt aag caa cgg tta tac	1344
Glu Asp Val Asp Leu Leu Lys Leu Ser Thr Arg Lys Gln Arg Leu Tyr	
430 435 440	
agg aaa aat acg gtg ggc tat tta ttt caa gat tat gcc ttg att ccc	1392
Arg Lys Asn Thr Val Gly Tyr Leu Phe Gln Asp Tyr Ala Leu Ile Pro	
445 450 455	
gac agg aca gtt aaa ttc aac ctt cag ctt gcg gtg gaa aaa cac aaa	1440
Asp Arg Thr Val Lys Phe Asn Leu Gln Leu Ala Val Glu Lys His Lys	
460 465 470 475	
tgg cct gaa att cct caa gta ctt cat gct gtt ggt ctt gag tcg ttc	1488
Trp Pro Glu Ile Pro Gln Val Leu His Ala Val Gly Leu Glu Ser Phe	
480 485 490	
gag gaa aag cca gtt ttt gaa ctc tct ggt ggc gaa caa caa cga act	1536
Glu Glu Lys Pro Val Phe Glu Leu Ser Gly Gly Glu Gln Gln Arg Thr	
495 500 505	
gcg ttg gcc cgg gta ctg ctc aaa aat ccc cga ata att ctg gct gat	1584
Ala Leu Ala Arg Val Leu Leu Lys Asn Pro Arg Ile Ile Leu Ala Asp	
510 515 520	
gaa cca acc gga gct cta gat tta aca aac agt gag cta gtc ata gaa	1632
Glu Pro Thr Gly Ala Leu Asp Leu Thr Asn Ser Glu Leu Val Ile Glu	
525 530 535	
gca ttg aga gca ctc gcc gac aaa ggc gcc acc gtt gtt gtt gct acg	1680
Ala Leu Arg Ala Leu Ala Asp Lys Gly Ala Thr Val Val Val Ala Thr	
540 545 550 555	
cac tcg ccc ctc ttc cga gaa tca gcg gat acc att atc aaa cta	1725

His Ser Pro Leu Phe Arg Glu Ser Ala Asp Thr Ile Ile Lys Leu	560	565	570	
taggtgcccc aacttttcg agatctcagt gca atg atg gaa ttc tta aac act				1779
		Met Met Glu Phe Leu Asn Thr	575	
cac cgt ttg att gtt ctc ggg agt ttg tct ttt cta ggg cta ggt ttc				1827
His Arg Leu Ile Val Leu Gly Ser Leu Ser Phe Leu Gly Leu Gly Phe	580	585	590	
gcg gaa gtc ctg ctg cgt ggc cag tgg tca aca ccg cag ttt ttt gtt				1875
Ala Glu Val Leu Leu Arg Gly Gln Trp Ser Thr Pro Gln Phe Phe Val	595	600	605	
ttc act ttc ttg caa act ctg ctt ctc gta ttg tgt ttt att cct aaa				1923
Phe Thr Phe Leu Gln Thr Leu Leu Leu Val Leu Cys Phe Ile Pro Lys	610	615	620	625
ctc tcg gtt cct ttt gtg gtg ctt cta agc att gcc caa ctc gcg ctt				1971
Leu Ser Val Pro Phe Val Val Leu Leu Ser Ile Ala Gln Leu Ala Leu		630	635	640
gca tac ctg tgt att cat ggt gaa cct caa agc acc agc cct ttc act				2019
Ala Tyr Leu Cys Ile His Gly Glu Pro Gln Ser Thr Ser Pro Phe Thr		645	650	655
tta att gtt gcc caa atg gcg ttt tcg gga ttg ctc atg ttc aga ggg				2067
Leu Ile Val Ala Gln Met Ala Phe Ser Gly Leu Leu Met Phe Arg Gly		660	665	670
caa cgg gtg ctc gct ttt atc tct gca ggt ggg ctc att tgg att ggg				2115
Gln Arg Val Leu Ala Phe Ile Ser Ala Gly Gly Leu Ile Trp Ile Gly	675	680	685	
acc atc gat cca aca aac ggt gct tgg tct cct cat gtg atg tcc gcg				2163
Thr Ile Asp Pro Thr Asn Gly Ala Trp Ser Pro His Val Met Ser Ala	690	695	700	705
cta gca ctt gcc gta ttc ttt gcg ctg tcg atg gca ctt gga cag gtt				2211
Leu Ala Leu Ala Val Phe Phe Ala Leu Ser Met Ala Leu Gly Gln Val		710	715	720
ctt cga tca aaa gtt gaa caa aga gcc aac ctt gag gag cag gca aaa				2259
Leu Arg Ser Lys Val Glu Gln Arg Ala Asn Leu Glu Glu Gln Ala Lys		725	730	735
att cag aca gaa ctg cgc aga aaa gaa cta agc act cca tct gca tcg				2307
Ile Gln Thr Glu Leu Arg Arg Lys Glu Leu Ser Thr Pro Ser Ala Ser		740	745	750
gtc ggt tgc caa aga act tac gtt tgc agt gat gaa atc gca gga gct				2355
Val Gly Cys Gln Arg Thr Tyr Val Cys Ser Asp Glu Ile Ala Gly Ala	755	760	765	
cag tgg tcg cga taa				2370
Gln Trp Ser Arg				

770

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<213> Brevibacterium lactofermentum .

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Gly Ser Leu Thr Gly Asn Leu Ser Glu Leu Arg Ala Gln Thr Thr Phe  
20 25 30

Ser Thr Leu Trp Asp Thr His Lys Glu Thr Tyr Arg Val Ser Ile Ala  
35 40 45

Ser Ala Ala Gly Gln Asp Phe Tyr Gly Leu Ala Glu Thr Leu Arg Thr  
50 55 60

Met Asp Arg His Gly Glu Ile Ile Leu Ala Asp Arg Gln Trp Leu Thr  
65 70 75 80

Ala Pro Leu Asp Ile Gly Ala Pro Val Val Leu Ser Asn Thr Thr Phe  
85 90 95

Ala Val Asp Glu Gly Leu Leu Ala Pro Lys Asp Leu Pro Gln Ser Asp  
100 105 110

Glu Ile Thr Ile Leu His Pro Gln Phe Leu Asp Ser Ala Lys Glu Pro  
115 120 125

Glu Leu Leu Gly Leu Leu Glu Phe Glu Ala Ser Asn Ser Gln Val Pro  
130 135 140

Met Pro Lys Ile Gln Ser Ile Pro Tyr Asp Ser Glu Asp Ser Thr Asn  
145 150 155 160

Pro Met Ser Glu Val Phe Thr Tyr Asn Ile Asn Leu Asp Ser Ala Val  
165 170 175

Arg Asn Pro Ile Val Val Ile Leu Pro Ala Gly Leu Glu Leu Leu Ser



09060338 061304

180	185	190
Asp Gln Asn Leu Ser Ala Arg Leu Thr Gln Asn Ser Leu Leu Ile Lys 195 200 205		
Asp Gln Thr Gly Val Asn Ala Leu Leu Ser Ser Glu Asp Ser Arg Asn 210 215 220		
Tyr Val Gly Ala Ala Ser Pro Met Ile Asp Thr Trp Glu Glu Ser Val 225 230 235 240		
Val Arg Leu Lys Glu Ala Asn Gln Ile Ile Ala Phe Asn Ala Phe Ile 245 250 255		
Ala Leu Phe Leu Thr Thr Thr Leu Val Leu Ala Tyr Cys Thr Gly Ile 260 265 270		
Ser Phe Lys Lys Ser Lys Lys Thr Met Gly Ser Ala Ser Thr Arg Lys 275 280 285		
Ser Ser Ile Lys Ser Ser Ile Thr Ala Ala Asn Cys Arg Ser Asn Phe 290 295 300		
Arg Phe Asn Ser Val Arg Leu Ala Arg Glu Pro Leu Phe Arg Ala Ile 305 310 315 320		
Cys Ser Asn Ser Phe Arg Cys Ser Leu Ser Gln Ile Leu Arg Thr Ser 325 330 335		
Gln Phe Tyr Thr Ser Ile Thr Ala Val Gly Phe Arg Asn Leu Asn Asn 340 345 350		
Arg Leu Asp Phe Thr Phe Ile Phe Gln Phe Asp Glu Ala Ser Phe 355 360 365		

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Ser Thr Pro Gln Phe Phe Val Phe Thr Phe Leu Gln Thr Leu Leu Leu  
35 40 45

Val Leu Cys Phe Ile Pro Lys Leu Ser Val Pro Phe Val Val Leu Leu  
50 55 60

Ser Ile Ala Gln Leu Ala Leu Ala Tyr Leu Cys Ile His Gly Glu Pro  
65 70 75 80

Gln Ser Thr Ser Pro Phe Thr Leu Ile Val Ala Gln Met Ala Phe Ser  
85 90 95

Gly Leu Leu Met Phe Arg Gly Gln Arg Val Leu Ala Phe Ile Ser Ala  
100 105 110

Gly Gly Leu Ile Trp Ile Gly Thr Ile Asp Pro Thr Asn Gly Ala Trp  
115 120 125

Ser Pro His Val Met Ser Ala Leu Ala Leu Ala Val Phe Phe Ala Leu  
130 135 140

Ser Met Ala Leu Gly Gln Val Leu Arg Ser Lys Val Glu Gln Arg Ala  
145 150 155 160

Asn Leu Glu Glu Gln Ala Lys Ile Gln Thr Glu Leu Arg Arg Lys Glu  
165 170 175

~~Leu Ser Thr Pro Ser Ala Ser Val Gly Cys Gln Arg Thr Tyr Val Cys~~  
~~180 185 190~~

Ser Asp Glu Ile Ala Gly Ala Gln Trp Ser Arg  
195 200